SEQUENCE LISTING

<110> Stegmann, Thomas
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Chernykh, Svitlana I
Vozianov, Oleksandr

<120> METHOD OF PRODUCING BIOLOGICALLY ACTIVE HUMAN ACIDIC FIBROBLAST GROWTH FACTOR AND ITS USE IN PROMOTING ANGIOGENESIS

<130> CVGENG.008CP1

<140> 10/649,480
<141> 2003-08-27

<150> 09/929,945
<151> 2001-08-15

<150> 60/225,406
<151> 2000-08-15

<150> 09/358,780
<151> 1999-07-22

<150> 60/093,962
<151> 1998-07-24

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized sequence for human acidic Fibroblast Growth Factor (155 amino acids) using preferred codons for E. coli

<221> CDS
<222> (122)...(590)

<400> 1
gcgtagagga tcgagatctc gatcccgcga aattaatacg actcactata ggggaattgt 60
gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatataca 120
t atg gct gaa ggg gaa atc acc acc ttt aca gcg tta acg gag aaa ttt 169
Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
1 5 10 15

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aac ctt ccg ccc ggg aat tac aaa aaa ccc aag ctt ctt tac tgc agt   217
Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
             20                  25                  30

aac gga gga cac ttc ctg cga att ctg cca gat ggc aca gta gat ggg   265
Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
         35                  40                  45

act cgc gat cgc tcc gac cag cac att cag ctg caa ctc tcg gcc gaa   313
Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
     50                  55                  60

agc gtt gga gag gtc tat atc aag tcg acg gag act ggc cag tac ctt   361
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
 65                  70                  75                  80

gcc atg gac acc gat ggg ctt ctg tat ggc tca cag acg cct aac gaa   409
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
                 85                  90                  95

gaa tgc ttg ttt cta gaa aga cta gaa gaa aac cat tac aac acg tac   457
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
            100                 105                 110

ata tcg aaa aaa cat gca gag aag aac tgg ttt gta ggc ctt aaa aaa   505
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
        115                 120                 125

aat ggt tcc tgt aag cgt gga cca cgg act cac tat ggc caa aag gct   553
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
    130                 135                 140

atc ttg ttc ctg cca cta cca gtg agc tcc gac taa g gatccgaatt      600
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp  *
145                 150                 155

cgagctccgt cgacaagctt gcggccgcac                                 630
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<210> 2
<211> 155
<212> PRT
<213> Homo sapiens

<400> 2

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Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
 1               5                  10                  15
Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
            20                  25                  30
Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
        35                  40                  45
Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
    50                  55                  60
Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
65                  70                  75                  80
Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
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```
                85                  90                  95
Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
            100                 105                 110
Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
        115                 120                 125
Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
    130                 135                 140
Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145                 150                 155
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<210> 3
<211> 468
<212> DNA
<213> Homo sapiens

<400> 3
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gggaattaca agaagcccaa actcctctac tgtagcaacg ggggccactt cctgaggatc 120
cttccggatg gcacagtgga tgggacaagg gacaggagcg accagcacat tcagctgcag 180
ctcagtgcgg aaagcgtggg ggaggtgtat ataaagagta ccgagactgg ccagtacttg 240
gccatggaca ccgacgggct tttatacggc tcacagacac caaatgagga atgtttgttc 300
ctggaaaggc tggaggagaa ccattacaac acctatatat ccaagaagca tgcagagaag 360
aattggtttg ttggcctcaa gaagaatggg agctgcaaac gcggtcctcg gactcactat 420
ggccagaaag caatcttgtt tctccccctg ccagtctctt ctgattaa 468

<210> 4
<211> 630
<212> DNA
<213> Artificial Sequence

<220>
<223> Chemically synthesized sequence for human acidic
Fibroblast Growth Factor (134 amino acids) using
preferred codons for E. coli

<221> CDS
<222> (122)...(526)

<400> 4
gcgtagagga tcgagatctc gatcccgcga aattaatacg actcactata ggggaattgt 60
gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatataca 120
t atg aat tac aaa aaa ccc aag ctt ctt tac tgc agt aac gga gga cac 169
  Met Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His
   1   5   10   15

ttc ctg cga att ctg cca gat ggc aca gta gat ggg act cgc gat cgc 217
Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg
            20   25   30

tcc gac cag cac att cag ctg caa ctc tcg gcc gaa agc gtt gga gag 265
Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu
        35   40   45

gtc tat atc aag tcg acg gag act ggc cag tac ctt gcc atg gac acc 313

```
Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr
     50                  55                  60

gat ggg ctt ctg tat ggc tca cag acg cct aac gaa gaa tgc ttg ttt   361
Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe
 65                  70                  75                  80

cta gaa aga cta gaa gaa aac cat tac aac acg tac ata tcg aaa aaa   409
Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys
                 85                  90                  95

cat gca gag aag aac tgg ttt gta ggc ctt aaa aaa aat ggt tcc tgt   457
His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys
            100                 105                 110

aag cgt gga cca cgg act cac tat ggc caa aag gct atc ttg ttc ctg   505
Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu
        115                 120                 125

cca cta cca gtg agc tcc gac taaggatccg aattcgagct ccgtcgacaa      556
Pro Leu Pro Val Ser Ser Asp
    130                 135

gcttgcggcc gcactcgagc accaccacca ccaccactga gatccggctg ctaacaaagc 616
ccgaaaggaa gctg                                                   630

<210> 5
<211> 135
<212> PRT
<213> Homo sapiens

<400> 5
Met Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His
 1               5                  10                  15
Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg
            20                  25                  30
Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu
        35                  40                  45
Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr
    50                  55                  60
Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe
65                  70                  75                  80
Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys
                85                  90                  95
His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys
            100                 105                 110
Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu
        115                 120                 125
Pro Leu Pro Val Ser Ser Asp
    130                 135


<210> 6
<211> 630
<212> DNA
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<213> Artificial Sequence

<220>
<223> Chemically synthesized sequence for human acidic
Fibroblast Growth Factor (140 amino acids) using
preferred codons for E. coli

<221> CDS
<222> (122)...(544)

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gcgtagagga tcgagatctc gatcccgcga aattaatacg actcactata ggggaattgt 60
gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatataca 120
t atg ttt aac ctt ccg ccc ggg aat tac aaa aaa ccc aag ctt ctt tac 169
Met Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
1 5 10 15

tgc agt aac gga gga cac ttc ctg cga att ctg cca gat ggc aca gta 217
Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
20 25 30

gat ggg act cgc gat cgc tcc gac cag cac att cag ctg caa ctc tcg 265
Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
35 40 45

gcc gaa agc gtt gga gag gtc tat atc aag tcg acg gag act ggc cag 313
Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
50 55 60

tac ctt gcc atg gac acc gat ggg ctt ctg tat ggc tca cag acg cct 361
Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
65 70 75 80

aac gaa gaa tgc ttg ttt cta gaa aga cta gaa gaa aac cat tac aac 409
Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
85 90 95

acg tac ata tcg aaa aaa cat gca gag aag aac tgg ttt gta ggc ctt 457
Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
100 105 110

aaa aaa aat ggt tcc tgt aag cgt gga cca cgg act cac tat ggc caa 505
Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
115 120 125

aag gct atc ttg ttc ctg cca cta cca gtg agc tcc gac taaggatccg 554
Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
130 135 140

aattcgagct ccgtcgacaa gcttgcggcc gcactcgagc accaccacca ccaccactga 614
gatccggctg ctaaca 630

<210> 7
<211> 141
<212> PRT

<213> Homo sapiens

<400> 7
Met Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
 1   5   10   15
Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
            20   25   30
Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
        35   40   45
Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
    50   55   60
Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
65   70   75   80
Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
                85   90   95
Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
            100   105   110
Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
        115   120   125
Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
    130   135   140

<210> 8
<211> 154
<212> PRT
<213> Homo sapiens

<400> 8
Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe Asn
 1   5   10   15
Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn
            20   25   30
Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr
        35   40   45
Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser
    50   55   60
Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala
65   70   75   80
Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu
                85   90   95
Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile
            100   105   110
Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn
        115   120   125
Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile
    130   135   140
Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
145   150